

SEQUENCE LISTING

<110> Godfrey, Wayne
Buck, David
Engleman, Edgar G.

<120> Receptor on the Surface of Activated T-Cells: ACT-4

<130> 16524.010

<150> US 08/472,940

<151> 1995-06-06

<150> US 08/147,784

<151> 1993-11-03

<160> 2

<210> 1

<211> 1058

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (15)..(845)

<220>

<223> ACT-4-h-1 cDNA

<400> 1

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		Met	Cys	Val	Gly	Ala	Arg	Arg	Leu	Gly	Arg	Gly	Pro	
		1				5					10			
tgt	gcg	gct	ctg	ctc	ctc	ctg	ggc	ctg	ggg	ctg	agc	acc	gtg	98
Cys	Ala	Ala	Leu	Leu	Leu	Leu	Gly	Leu	Gly	Leu	Ser	Thr	Val	
	15					20					25			
ctc	cac	tgt	gtc	ggg	gac	acc	tac	ccc	agc	aac	gac	cgg	tgc	146
Leu	His	Cys	Val	Gly	Asp	Thr	Tyr	Pro	Ser	Asn	Asp	Arg	Cys	
	30				35						40			
gag	tgc	agg	cca	ggc	aac	ggg	atg	gtg	agc	cgc	tgc	agc	cgc	194
Glu	Cys	Arg	Pro	Gly	Asn	Gly	Met	Val	Ser	Arg	Cys	Ser	Arg	
	45			50					55				60	
aac	acg	gtg	tgc	cgt	ccg	tgc	ggg	ccg	ggc	ttc	tac	aac	gac	242
Asn	Thr	Val	Cys	Arg	Pro	Cys	Gly	Pro	Gly	Phe	Tyr	Asn	Asp	
			65				70						75	
agc	tcc	aag	ccg	tgc	aag	ccc	tgc	acg	tgg	tgt	aac	ctc	aga	290
Ser	Ser	Lys	Pro	Cys	Lys	Pro	Cys	Thr	Trp	Cys	Asn	Leu	Arg	
		80					85					90		
agt	gag	cgg	aag	cag	ctg	tgc	acg	gcc	aca	cag	gac	aca	gtc	338

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Ser	Glu	Arg	Lys	Gln	Leu	Cys	Thr	Ala	Thr	Gln	Asp	Thr	Val	Cys	Arg	
	95						100					105				
tgc	cgg	gcg	ggc	acc	cag	ccc	ctg	gac	agc	tac	aag	cct	gga	gtt	gac	386
Cys	Arg	Ala	Gly	Thr	Gln	Pro	Leu	Asp	Ser	Tyr	Lys	Pro	Gly	Val	Asp	
	110					115					120					
tgt	gcc	ccc	tgc	cct	cca	ggg	cac	ttc	ttc	cca	ggc	gac	aac	cag	gcc	434
Cys	Ala	Pro	Cys	Pro	Pro	Gly	His	Phe	Ser	Pro	Gly	Asp	Asn	Gln	Ala	
	125				130					135					140	
tgc	aag	ccc	tgg	acc	aac	tgc	acc	ttg	gct	ggg	aag	cac	acc	ctg	cag	482
Cys	Lys	Pro	Trp	Thr	Asn	Cys	Thr	Leu	Ala	Gly	Lys	His	Thr	Leu	Gln	
				145					150					155		
ccg	gcc	agc	aat	agc	tgc	gac	gca	atc	tgt	gag	gac	agg	gac	ccc	cca	530
Pro	Ala	Ser	Asn	Ser	Ser	Asp	Ala	Ile	Cys	Glu	Asp	Arg	Asp	Pro	Pro	
			160					165					170			
gcc	acg	cag	ccc	cag	gag	acc	cag	ggc	ccc	ccg	gcc	agg	ccc	atc	act	578
Ala	Thr	Gln	Pro	Gln	Glu	Thr	Gln	Gly	Pro	Pro	Ala	Arg	Pro	Ile	Thr	
		175					180					185				
gtc	cag	ccc	act	gaa	gcc	tgg	ccc	aga	acc	tca	cag	gga	ccc	tcc	acc	626
Val	Gln	Pro	Thr	Glu	Ala	Trp	Pro	Arg	Thr	Ser	Gln	Gly	Pro	Ser	Thr	
	190					195					200					
cgg	ccc	gtg	gag	gtc	ccc	ggg	ggc	cgt	gcg	gtt	gcc	gcc	atc	ctg	ggc	674
Arg	Pro	Val	Glu	Val	Pro	Gly	Gly	Arg	Ala	Val	Ala	Ala	Ile	Leu	Gly	
	205				210					215				220		
ctg	ggc	ctg	gtg	ctg	ggg	ctg	ctg	ggc	ccc	ctg	gcc	atc	ctg	ctg	gcc	722
Leu	Gly	Leu	Val	Leu	Gly	Leu	Leu	Gly	Pro	Leu	Ala	Ile	Leu	Leu	Ala	
				225					230					235		
ctg	tac	ctg	ctc	cgg	agg	gac	cag	agg	ctg	ccc	ccc	gat	gcc	cac	aag	770
Leu	Tyr	Leu	Leu	Arg	Arg	Asp	Gln	Arg	Leu	Pro	Pro	Asp	Ala	His	Lys	
			240				245						250			
ccc	cct	ggg	gga	ggc	agt	ttc	cgg	acc	ccc	atc	caa	gag	gag	cag	gcc	818
Pro	Pro	Gly	Gly	Gly	Ser	Phe	Arg	Thr	Pro	Ile	Gln	Glu	Glu	Gln	Ala	
	255					260						265				
gac	gcc	cac	tcc	acc	ctg	gcc	aag	atc	tgac	ctt	gggc	ccacca	aggt			866
Asp	Ala	His	Ser	Thr	Leu	Ala	Lys	Ile								
	270					275										
ggacgctggg	ccccgccagg	ctggagcccg	gagggctctgc	tgggcgagca	gggcaggtgc											926
aggccgcctg	ccccgccacg	ctcctgggcc	aactctgcac	cgttctaggt	gccgatggct											986
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aaaccttggc	ag															1058

<211> 277
 <212> PRT
 <213> Homo sapiens

<220>
 <223> deduced amino acid sequence of ACT-4-h-1

<400> 2

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Leu	Leu	Leu	Gly	Leu	Gly	Leu	Ser	Thr	Val	Thr	Gly	Leu	His	Cys	Val	20	25	30	
Gly	Asp	Thr	Tyr	Pro	Ser	Asn	Asp	Arg	Cys	Cys	His	Glu	Cys	Arg	Pro	35	40	45	
Gly	Asn	Gly	Met	Val	Ser	Arg	Cys	Ser	Arg	Ser	Gln	Asn	Thr	Val	Cys	50	55	60	
Arg	Pro	Cys	Gly	Pro	Gly	Phe	Tyr	Asn	Asp	Val	Val	Ser	Ser	Lys	Pro	65	70	75	80
Cys	Lys	Pro	Cys	Thr	Trp	Cys	Asn	Leu	Arg	Ser	Gly	Ser	Glu	Arg	Lys	85	90	95	
Gln	Leu	Cys	Thr	Ala	Thr	Gln	Asp	Thr	Val	Cys	Arg	Cys	Arg	Ala	Gly	100	105	110	
Thr	Gln	Pro	Leu	Asp	Ser	Tyr	Lys	Pro	Gly	Val	Asp	Cys	Ala	Pro	Cys	115	120	125	
Pro	Pro	Gly	His	Phe	Ser	Pro	Gly	Asp	Asn	Gln	Ala	Cys	Lys	Pro	Trp	130	135	140	
Thr	Asn	Cys	Thr	Leu	Ala	Gly	Lys	His	Thr	Leu	Gln	Pro	Ala	Ser	Asn	145	150	155	160
Ser	Ser	Asp	Ala	Ile	Cys	Glu	Asp	Arg	Asp	Pro	Pro	Ala	Thr	Gln	Pro	165	170	175	
Gln	Glu	Thr	Gln	Gly	Pro	Pro	Ala	Arg	Pro	Ile	Thr	Val	Gln	Pro	Thr	180	185	190	
Glu	Ala	Trp	Pro	Arg	Thr	Ser	Gln	Gly	Pro	Ser	Thr	Arg	Pro	Val	Glu	195	200	205	
Val	Pro	Gly	Gly	Arg	Ala	Val	Ala	Ala	Ile	Leu	Gly	Leu	Gly	Leu	Val	210	215	220	
Leu	Gly	Leu	Leu	Gly	Pro	Leu	Ala	Ile	Leu	Leu	Ala	Leu	Tyr	Leu	Leu	225	230	235	240
Arg	Arg	Asp	Gln	Arg	Leu	Pro	Pro	Asp	Ala	His	Lys	Pro	Pro	Gly	Gly	245	250	255	

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Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
260 265 270

Thr Leu Ala Lys Ile
275

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